



SEQUENCE LISTING

<110> Mather, Jennie P.
Bald, Laura N.
Roberts, Penelope E.
Stephan, Jean-Philippe F.

<120> COMPOSITIONS AND METHODS FOR GENERATING
MONOCLONAL ANTIBODIES REPRESENTATIVE OF A SPECIFIC CELL TYPE

<130> 415072000110

<140> 09/614,483

<141> 2000-07-10

<150> 09/218,539

<151> 1998-12-22

<160> 8

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2181

<212> DNA

<213> Rattus rattus

<220>

<221> sig_peptide

<222> (0)...(454)

<221> CDS

<222> (454)...(2181)

<400> 1

cac ctc ggt tct atc gat tcg aat tcg gcc aca ctg gcc gga tcc tct 48
His Leu Gly Ser Ile Asp Ser Asn Ser Ala Thr Leu Ala Gly Ser Ser
-150 -145 -140

aga gat ccc tcg acc tcg acc cac gcg tcc gcc ttg ctc ttc tta tcc 96
Arg Asp Pro Ser Thr Ser Thr His Ala Ser Ala Leu Leu Phe Leu Ser
-135 -130 -125 -120

tct cct ttg caa gaa gag aaa ctc ctc gga gac agc agc caa aaa gaa 144
Ser Pro Leu Gln Glu Lys Leu Leu Gly Asp Ser Ser Gln Lys Glu
-115 -110 -105

acc gcg tct acc ttg aca gac tac tga agc gtc tcc tgg aat aag agg 192
Thr Ala Ser Thr Leu Thr Asp Tyr * Ser Val Ser Trp Asn Lys Arg
-100 -95 -90

gtc gcc cgc ctt ggg agt agc agc caa aga cgc tga ggg agg gtg tgg 240
Val Ala Arg Leu Gly Ser Ser Ser Gln Arg Arg * Gly Arg Val Trp
-85 -80 -75

agg ggg gag gga gga gtt gcg ggt tcc gcg tgg agg aaa gtt gcg tgt	288
Arg Gly Glu Gly Gly Val Ala Gly Ser Ala Trp Arg Lys Val Ala Cys	
-70 -65 -60	
ggc aca gac ccg acg gcg cag cgc cac agc gcc cgg ggg atc gtg tgt	336
Gly Thr Asp Pro Thr Ala Gln Arg His Ser Ala Arg Gly Ile Val Cys	
-55 -50 -45	
ctt gga aaa aaa agt cgc tgt ccc cct aaa gcg aga ccc aca agc gag	384
Leu Gly Lys Lys Ser Arg Cys Pro Pro Lys Ala Arg Pro Thr Ser Glu	
-40 -35 -30	
cgg gcc ccg tgg gcc cgg gga cga cgc ccc ctc ctg cgg cgt gga ctt	432
Arg Ala Pro Trp Ala Arg Gly Arg Arg Pro Leu Leu Arg Arg Gly Leu	
-25 -20 -15 -10	
tgt cgg tgg cct tct agg agg agg aat atg gca tct aaa ggg tcc cct	480
Cys Arg Trp Pro Ser Arg Arg Arg Asn Met Ala Ser Lys Gly Ser Pro	
-5 1 5	
tct tgc cgt ctg gtt ttc tgc ctc ttg atc tcc gcc gcg gtc ctc aga	528
Ser Cys Arg Leu Val Phe Cys Leu Leu Ile Ser Ala Ala Val Leu Arg	
10 15 20	
cca ggc ctc gga tgg tac act gtc aac tca gca tac gga gat acc att	576
Pro Gly Leu Gly Trp Tyr Thr Val Asn Ser Ala Tyr Gly Asp Thr Ile	
25 30 35	
gtc atg cct tgc aga ctg gat gta cct cag aac ctc atg ttt ggc aaa	624
Val Met Pro Cys Arg Leu Asp Val Pro Gln Asn Leu Met Phe Gly Lys	
40 45 50 55	
tgg aaa tat gaa aag cct gat ggg tcc cca gta ttt att gca ttc aga	672
Trp Lys Tyr Glu Lys Pro Asp Gly Ser Pro Val Phe Ile Ala Phe Arg	
60 65 70	
tct tct aca aag aaa agt gtg cag tat gat gat gta cca gag tac aag	720
Ser Ser Thr Lys Lys Ser Val Gln Tyr Asp Asp Val Pro Glu Tyr Lys	
75 80 85	
gac aga ctg agc ctc tca gaa aac tac act ctg tct atc aac aat gca	768
Asp Arg Leu Ser Leu Ser Glu Asn Tyr Thr Leu Ser Ile Asn Asn Ala	
90 95 100	
aag atc agt gac gaa aag aga ttt gtg tgc atg cta gtg acc gag gac	816
Lys Ile Ser Asp Glu Lys Arg Phe Val Cys Met Leu Val Thr Glu Asp	
105 110 115	
aac gtg ttt gag gca cct acc ctg gtc aag gtg ttc aag caa cca tct	864
Asn Val Phe Glu Ala Pro Thr Leu Val Lys Val Phe Lys Gln Pro Ser	
120 125 130 135	
aaa cct gaa att gta aac aga gca gcg ttt ctt gaa aca gag cag cta	912
Lys Pro Glu Ile Val Asn Arg Ala Ala Phe Leu Glu Thr Glu Gln Leu	
140 145 150	
aaa aag tta ggt gac tgc att tca aga gac agt tac cca gac ggc aac	960

Lys	Lys	Leu	Gly	Asp	Cys	Ile	Ser	Arg	Asp	Ser	Tyr	Pro	Asp	Gly	Asn		
			155					160					165				
atc	acg	tgg	tat	agg	aat	ggg	aaa	gtg	cta	cag	cct	gtt	gat	gga	gag	1008	
Ile	Thr	Trp	Tyr	Arg	Asn	Gly	Lys	Val	Leu	Gln	Pro	Val	Asp	Gly	Glu		
		170					175					180					
gtg	tcc	ata	ctt	ttt	aaa	aag	gaa	att	gat	cca	ggg	act	cag	ttg	tat	1056	
Val	Ser	Ile	Leu	Phe	Lys	Lys	Glu	Ile	Asp	Pro	Gly	Thr	Gln	Leu	Tyr		
	185					190					195						
acc	atg	act	tcc	tcc	ttg	gag	tac	aag	aca	acc	aag	tct	gac	ata	caa	1104	
Thr	Met	Thr	Ser	Ser	Leu	Glu	Tyr	Lys	Thr	Thr	Lys	Ser	Asp	Ile	Gln		
200					205					210					215		
atg	cca	ttc	acc	tgt	tct	gtg	aca	tat	tat	gga	cct	tcg	ggc	cag	aaa	1152	
Met	Pro	Phe	Thr	Cys	Ser	Val	Thr	Tyr	Tyr	Gly	Pro	Ser	Gly	Gln	Lys		
				220				225						230			
aca	att	tat	tct	gaa	caa	gca	atc	ttt	gat	att	tac	tat	cct	aca	gag	1200	
Thr	Ile	Tyr	Ser	Glu	Gln	Ala	Ile	Phe	Asp	Ile	Tyr	Tyr	Pro	Thr	Glu		
			235				240						245				
cag	gtg	aca	ata	caa	gta	ctg	cca	cca	aaa	aat	gcc	atc	aaa	gaa	ggg	1248	
Gln	Val	Thr	Ile	Gln	Val	Leu	Pro	Pro	Lys	Asn	Ala	Ile	Lys	Glu	Gly		
		250				255					260						
gac	aac	atc	acc	ctt	cag	tgc	ttg	ggg	aat	ggc	aac	cca	cct	cct	gag	1296	
Asp	Asn	Ile	Thr	Leu	Gln	Cys	Leu	Gly	Asn	Gly	Asn	Pro	Pro	Pro	Glu		
	265					270				275							
gag	ttc	atg	ttt	tac	tta	cca	ggg	cag	gct	gaa	ggc	ata	aga	agc	tca	1344	
Glu	Phe	Met	Phe	Tyr	Leu	Pro	Gly	Gln	Ala	Glu	Gly	Ile	Arg	Ser	Ser		
280					285					290					295		
aac	act	tac	aca	ctg	aca	gac	gtg	aga	cgc	aat	gcc	acc	ggg	gac	tac	1392	
Asn	Thr	Tyr	Thr	Leu	Thr	Asp	Val	Arg	Arg	Asn	Ala	Thr	Gly	Asp	Tyr		
				300				305					310				
aaa	tgt	tct	ctc	atc	gac	caa	aga	aac	atg	gca	gct	tca	aca	acc	atc	1440	
Lys	Cys	Ser	Leu	Ile	Asp	Gln	Arg	Asn	Met	Ala	Ala	Ser	Thr	Thr	Ile		
			315				320					325					
act	gtt	cac	tac	ttg	gat	tta	tcc	tta	aac	cca	agt	ggg	gaa	gtg	acc	1488	
Thr	Val	His	Tyr	Leu	Asp	Leu	Ser	Leu	Asn	Pro	Ser	Gly	Glu	Val	Thr		
		330				335						340					
aag	cag	atc	ggg	gat	acc	ctg	cct	gtg	tct	tgc	aca	ata	tct	gca	agt	1536	
Lys	Gln	Ile	Gly	Asp	Thr	Leu	Pro	Val	Ser	Cys	Thr	Ile	Ser	Ala	Ser		
	345					350					355						
agg	aat	gca	act	gtg	gtg	tgg	atg	aag	gat	aac	atc	agg	ctc	cga	tct	1584	
Arg	Asn	Ala	Thr	Val	Val	Trp	Met	Lys	Asp	Asn	Ile	Arg	Leu	Arg	Ser		
360					365					370					375		
agt	cca	tcc	ttt	tct	agt	ctt	cat	tat	cag	gat	gct	ggg	aac	tat	gtc	1632	
Ser	Pro	Ser	Phe	Ser	Ser	Leu	His	Tyr	Gln	Asp	Ala	Gly	Asn	Tyr	Val		

B.

	380	385	390	
	tgt gaa act gct ctt cag gag gtt	gag gga ctg aag aaa agg gag tcg	1680	
	Cys Glu Thr Ala Leu Gln Glu Val	Glu Gly Leu Lys Lys Arg Glu Ser		
	395	400	405	
	ctg acc ctc atc gta gaa gga aaa	cct caa atc aaa atg aca aag aaa	1728	
	Leu Thr Leu Ile Val Glu Gly Lys	Pro Gln Ile Lys Met Thr Lys Lys		
	410	415	420	
	act gat ccc agt gga ctg tct aag	act ata atc tgc cat gtg gaa ggg	1776	
	Thr Asp Pro Ser Gly Leu Ser Lys	Thr Ile Ile Cys His Val Glu Gly		
	425	430	435	
	ttt cca aag cca gct ata cag tgg	acc att acc ggc agt gga agc gtc	1824	
	Phe Pro Lys Pro Ala Ile Gln Trp	Thr Ile Thr Gly Ser Gly Ser Val		
	440	445	450	
	ata aac caa aca gag gag tct cct	tat att aat ggc agg tat tat agt	1872	
	Ile Asn Gln Thr Glu Glu Ser Pro	Tyr Ile Asn Gly Arg Tyr Tyr Ser		
	460	465	470	
	aaa att atc att tcc cct gag gag	aat gtt aca tta act tgc aca gca	1920	
	Lys Ile Ile Ile Ser Pro Glu Glu	Asn Val Thr Leu Thr Cys Thr Ala		
	475	480	485	
	gaa aac caa ctg gag aga aca gta	aac tcc ctg aat gtc tct gcg ata	1968	
	Glu Asn Gln Leu Glu Arg Thr Val	Asn Ser Leu Asn Val Ser Ala Ile		
	490	495	500	
B ₁	agt att cca gaa cac gat gag gca	gac gat ata agt gat gaa aat aga	2016	
	Ser Ile Pro Glu His Asp Glu Ala	Asp Asp Ile Ser Asp Glu Asn Arg		
	505	510	515	
	gaa aag gtg aat gac cag gcc aaa	cta att gtg ggc att gtg gtt ggt	2064	
	Glu Lys Val Asn Asp Gln Ala Lys	Leu Ile Val Gly Ile Val Val Gly		
	520	525	530	
	ctc ctc ctc gcc gcc ctc gtc gcc	ggt gtc gtc tac tgg ctg tac atg	2112	
	Leu Leu Leu Ala Ala Leu Val Ala	Gly Val Val Tyr Trp Leu Tyr Met		
	540	545	550	
	aag aaa tcg aaa act gca tca aaa	cat gca aaa aaa aaa aaa aaa aaa	2160	
	Lys Lys Ser Lys Thr Ala Ser Lys	His Ala Lys Lys Lys Lys Lys Lys		
	555	560	565	
	aaa aaa aag ggc ggc cgc gac		2181	
	Lys Lys Lys Gly Gly Arg Asp			
	570			

<210> 2
 <211> 725
 <212> PRT
 <213> Rattus rattus
 <220>

<221> SIGNAL
 <222> (1)...(152)

<400> 2

His Leu Gly Ser Ile Asp Ser Asn Ser Ala Thr Leu Ala Gly Ser Ser
 -150 -145 -140
 Arg Asp Pro Ser Thr Ser Thr His Ala Ser Ala Leu Leu Phe Leu Ser
 -135 -130 -125
 Ser Pro Leu Gln Glu Glu Lys Leu Leu Gly Asp Ser Ser Gln Lys Glu
 -120 -115 -110 -105
 Thr Ala Ser Thr Leu Thr Asp Tyr Ser Val Ser Trp Asn Lys Arg Val
 -100 -95 -90
 Ala Arg Leu Gly Ser Ser Ser Gln Arg Arg Gly Arg Val Trp Arg Gly
 -85 -80 -75
 Glu Gly Gly Val Ala Gly Ser Ala Trp Arg Lys Val Ala Cys Gly Thr
 -70 -65 -60
 Asp Pro Thr Ala Gln Arg His Ser Ala Arg Gly Ile Val Cys Leu Gly
 -55 -50 -45
 Lys Lys Ser Arg Cys Pro Pro Lys Ala Arg Pro Thr Ser Glu Arg Ala
 -40 -35 -30 -25
 Pro Trp Ala Arg Gly Arg Arg Pro Leu Leu Arg Arg Gly Leu Cys Arg
 -20 -15 -10
 Trp Pro Ser Arg Arg Arg Asn Met Ala Ser Lys Gly Ser Pro Ser Cys
 -5 1 5
 Arg Leu Val Phe Cys Leu Leu Ile Ser Ala Ala Val Leu Arg Pro Gly
 10 15 20
 Leu Gly Trp Tyr Thr Val Asn Ser Ala Tyr Gly Asp Thr Ile Val Met
 25 30 35 40
 Pro Cys Arg Leu Asp Val Pro Gln Asn Leu Met Phe Gly Lys Trp Lys
 45 50 55
 Tyr Glu Lys Pro Asp Gly Ser Pro Val Phe Ile Ala Phe Arg Ser Ser
 60 65 70
 Thr Lys Lys Ser Val Gln Tyr Asp Asp Val Pro Glu Tyr Lys Asp Arg
 75 80 85
 Leu Ser Leu Ser Glu Asn Tyr Thr Leu Ser Ile Asn Asn Ala Lys Ile
 90 95 100
 Ser Asp Glu Lys Arg Phe Val Cys Met Leu Val Thr Glu Asp Asn Val
 105 110 115 120
 Phe Glu Ala Pro Thr Leu Val Lys Val Phe Lys Gln Pro Ser Lys Pro
 125 130 135
 Glu Ile Val Asn Arg Ala Ala Phe Leu Glu Thr Glu Gln Leu Lys Lys
 140 145 150
 Leu Gly Asp Cys Ile Ser Arg Asp Ser Tyr Pro Asp Gly Asn Ile Thr
 155 160 165
 Trp Tyr Arg Asn Gly Lys Val Leu Gln Pro Val Asp Gly Glu Val Ser
 170 175 180
 Ile Leu Phe Lys Lys Glu Ile Asp Pro Gly Thr Gln Leu Tyr Thr Met
 185 190 195 200
 Thr Ser Ser Leu Glu Tyr Lys Thr Thr Lys Ser Asp Ile Gln Met Pro
 205 210 215
 Phe Thr Cys Ser Val Thr Tyr Tyr Gly Pro Ser Gly Gln Lys Thr Ile
 220 225 230
 Tyr Ser Glu Gln Ala Ile Phe Asp Ile Tyr Tyr Pro Thr Glu Gln Val
 235 240 245
 Thr Ile Gln Val Leu Pro Pro Lys Asn Ala Ile Lys Glu Gly Asp Asn
 250 255 260
 Ile Thr Leu Gln Cys Leu Gly Asn Gly Asn Pro Pro Pro Glu Glu Phe

B₁

265 270 275 280
 Met Phe Tyr Leu Pro Gly Gln Ala Glu Gly Ile Arg Ser Ser Asn Thr
 285 290 295
 Tyr Thr Leu Thr Asp Val Arg Arg Asn Ala Thr Gly Asp Tyr Lys Cys
 300 305 310
 Ser Leu Ile Asp Gln Arg Asn Met Ala Ala Ser Thr Thr Ile Thr Val
 315 320 325
 His Tyr Leu Asp Leu Ser Leu Asn Pro Ser Gly Glu Val Thr Lys Gln
 330 335 340
 Ile Gly Asp Thr Leu Pro Val Ser Cys Thr Ile Ser Ala Ser Arg Asn
 345 350 355 360
 Ala Thr Val Val Trp Met Lys Asp Asn Ile Arg Leu Arg Ser Ser Pro
 365 370 375
 Ser Phe Ser Ser Leu His Tyr Gln Asp Ala Gly Asn Tyr Val Cys Glu
 380 385 390
 Thr Ala Leu Gln Glu Val Glu Gly Leu Lys Lys Arg Glu Ser Leu Thr
 395 400 405
 Leu Ile Val Glu Gly Lys Pro Gln Ile Lys Met Thr Lys Lys Thr Asp
 410 415 420
 Pro Ser Gly Leu Ser Lys Thr Ile Ile Cys His Val Glu Gly Phe Pro
 425 430 435 440
 Lys Pro Ala Ile Gln Trp Thr Thr Ile Thr Gly Ser Gly Ser Val Ile Asn
 445 450 455
 Gln Thr Glu Glu Ser Pro Tyr Ile Asn Gly Arg Tyr Tyr Ser Lys Ile
 460 465 470
 Ile Ile Ser Pro Glu Glu Asn Val Thr Leu Thr Cys Thr Ala Glu Asn
 475 480 485
 Gln Leu Glu Arg Thr Val Asn Ser Leu Asn Val Ser Ala Ile Ser Ile
 490 495 500
 Pro Glu His Asp Glu Ala Asp Asp Ile Ser Asp Glu Asn Arg Glu Lys
 505 510 515 520
 Val Asn Asp Gln Ala Lys Leu Ile Val Gly Ile Val Val Gly Leu Leu
 525 530 535
 Leu Ala Ala Leu Val Ala Gly Val Val Tyr Trp Leu Tyr Met Lys Lys
 540 545 550
 Ser Lys Thr Ala Ser Lys His Ala Lys Lys Lys Lys Lys Lys Lys Lys
 555 560 565
 Lys Gly Gly Arg Asp
 570

<210> 3
 <211> 1291
 <212> DNA
 <213> Rattus rattus

<220>
 <221> CDS
 <222> (134)...(1078)

<400> 3

ctctagagat ccctcgacct cgaccacgc gtccggcgca gaggcgtcag tcggtcggcc 60
 gccgtgcagc ggcactgtcc ctggagccgt cccgcgcctc agaccgcga gtccccgccg 120
 ctccgcgcgc agt atg gcg ccc ccc aag gcc ctc gcg ttc ggg ctc ctg 169
 Met Ala Pro Pro Lys Ala Leu Ala Phe Gly Leu Leu
 1 5 10

ctc gcg gtg gtc acg gcg acg ctg gcc gca gct cag aaa gac tgt gtc 217

Leu	Ala	Val	Val	Thr	Ala	Thr	Leu	Ala	Ala	Ala	Gln	Lys	Asp	Cys	Val		
		15					20					25					
tgt	aac	aac	tac	aag	ctg	acg	tca	cgg	tgc	tat	gag	aat	gag	aat	ggg	265	
Cys	Asn	Asn	Tyr	Lys	Leu	Thr	Ser	Arg	Cys	Tyr	Glu	Asn	Glu	Asn	Gly		
	30					35					40						
gaa	tgc	cag	tgt	act	tcc	tat	ggg	aca	caa	aat	act	gtc	att	tgc	tcc	313	
Glu	Cys	Gln	Cys	Thr	Ser	Tyr	Gly	Thr	Gln	Asn	Thr	Val	Ile	Cys	Ser		
	45				50					55					60		
aaa	ctg	gca	tcc	aag	tgc	ttg	gtg	atg	aag	gcg	gag	atg	act	cac	agc	361	
Lys	Leu	Ala	Ser	Lys	Cys	Leu	Val	Met	Lys	Ala	Glu	Met	Thr	His	Ser		
				65					70					75			
aag	tct	ggg	agg	agg	atg	aaa	ccc	gag	ggg	gcg	atc	cag	aac	aac	gac	409	
Lys	Ser	Gly	Arg	Arg	Met	Lys	Pro	Glu	Gly	Ala	Ile	Gln	Asn	Asn	Asp		
			80					85					90				
ggg	ctg	tat	gat	ccc	gag	tgt	gac	gag	caa	ggg	ctc	ttc	aaa	gcc	aag	457	
Gly	Leu	Tyr	Asp	Pro	Glu	Cys	Asp	Glu	Gln	Gly	Leu	Phe	Lys	Ala	Lys		
		95					100					105					
cag	tgc	aac	ggc	acc	gcc	acg	tgc	tgg	tgc	gtg	aac	acc	gcg	ggg	gtc	505	
Gln	Cys	Asn	Gly	Thr	Ala	Thr	Cys	Trp	Cys	Val	Asn	Thr	Ala	Gly	Val		
	110					115					120						
cgg	aga	acc	gac	aag	gac	acg	gag	atc	acg	tgc	tcc	gag	aga	gtg	agg	553	
Arg	Arg	Thr	Asp	Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg		
	125				130					135					140		
acc	tac	tgg	atc	atc	att	gag	ctc	aaa	cac	aaa	gaa	aga	gca	cag	cct	601	
Thr	Tyr	Trp	Ile	Ile	Ile	Glu	Leu	Lys	His	Lys	Glu	Arg	Ala	Gln	Pro		
				145					150					155			
tat	aac	ttc	gag	agt	ttg	cat	act	gca	ctt	cag	gac	aca	ttt	gca	tct	649	
Tyr	Asn	Phe	Glu	Ser	Leu	His	Thr	Ala	Leu	Gln	Asp	Thr	Phe	Ala	Ser		
			160					165					170				
cga	tac	atg	ctg	aat	ccg	aaa	ttt	atc	aaa	agt	att	atg	tat	gag	aat	697	
Arg	Tyr	Met	Leu	Asn	Pro	Lys	Phe	Ile	Lys	Ser	Ile	Met	Tyr	Glu	Asn		
		175					180					185					
aat	gtt	atc	act	att	gat	ttg	atg	caa	aac	tct	tct	cag	aag	act	caa	745	
Asn	Val	Ile	Thr	Ile	Asp	Leu	Met	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln		
	190					195					200						
gat	gat	gtg	gac	ata	gct	gat	gtg	gct	tac	tat	ttt	gag	aaa	gat	gta	793	
Asp	Asp	Val	Asp	Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val		
	205				210					215					220		
aag	ggg	gag	tcc	ttg	ttc	cat	tca	tct	aag	agc	atg	gac	ctg	agg	gtg	841	
Lys	Gly	Glu	Ser	Leu	Phe	His	Ser	Ser	Lys	Ser	Met	Asp	Leu	Arg	Val		
				225					230				235				
aac	ggg	gag	ctc	ctc	gat	ctg	gac	ccc	ggg	cag	act	ctg	att	tac	tac	889	
Asn	Gly	Glu	Leu	Leu	Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr		

240	245	250	
gtc gat gaa aag gcc ccg gag ttt tcc atg cag ggc ctc acg gct ggg			937
Val Asp Glu Lys Ala Pro Glu Phe Ser Met Gln Gly Leu Thr Ala Gly			
255	260	265	
atc atc gcc gtc att gtc gtg gtg gtg tta gca gtc att gcg ggg att			985
Ile Ile Ala Val Ile Val Val Val Val Leu Ala Val Ile Ala Gly Ile			
270	275	280	
gtt gtc ctg gtt ata tct aca agg aag aga tca gca aaa tat gag aag			1033
Val Val Leu Val Ile Ser Thr Arg Lys Arg Ser Ala Lys Tyr Glu Lys			
285	290	295	300
gct gag ata aag gag atg ggt gag ata cac aga gag ctc aat gcc			1078
Ala Glu Ile Lys Glu Met Gly Glu Ile His Arg Glu Leu Asn Ala			
305	310	315	
taaccaacca tgccgtgtgc tgcaactgagg agggagccac cggacggaaa tggcgaagaa			1138
ctcaggttgc aaacggatag acctggggag gatggagacc ttctgagggt cactgctttg			1198
ttagctaagc tcacacattt gtaacagtga aatttgtact cataaatata agcagcttga			1258
cattggcaaaa aaaaaaaaaa aaaaaaaaaa agg			1291

<210> 4
 <211> 315
 <212> PRT
 <213> Rattus rattus

<400> 4

B.

Met Ala Pro Pro Lys Ala Leu Ala Phe Gly Leu Leu Leu Ala Val Val			
1	5	10	15
Thr Ala Thr Leu Ala Ala Ala Gln Lys Asp Cys Val Cys Asn Asn Tyr			
20	25	30	
Lys Leu Thr Ser Arg Cys Tyr Glu Asn Glu Asn Gly Glu Cys Gln Cys			
35	40	45	
Thr Ser Tyr Gly Thr Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ser			
50	55	60	
Lys Cys Leu Val Met Lys Ala Glu Met Thr His Ser Lys Ser Gly Arg			
65	70	75	80
Arg Met Lys Pro Glu Gly Ala Ile Gln Asn Asn Asp Gly Leu Tyr Asp			
85	90	95	
Pro Glu Cys Asp Glu Gln Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly			
100	105	110	
Thr Ala Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Thr Asp			
115	120	125	
Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile			
130	135	140	
Ile Ile Glu Leu Lys His Lys Glu Arg Ala Gln Pro Tyr Asn Phe Glu			
145	150	155	160
Ser Leu His Thr Ala Leu Gln Asp Thr Phe Ala Ser Arg Tyr Met Leu			
165	170	175	
Asn Pro Lys Phe Ile Lys Ser Ile Met Tyr Glu Asn Asn Val Ile Thr			
180	185	190	
Ile Asp Leu Met Gln Asn Ser Ser Gln Lys Thr Gln Asp Asp Val Asp			
195	200	205	
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser			
210	215	220	

Leu Phe His Ser Ser Lys Ser Met Asp Leu Arg Val Asn Gly Glu Leu
 225 230 235 240
 Leu Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys
 245 250 255
 Ala Pro Glu Phe Ser Met Gln Gly Leu Thr Ala Gly Ile Ile Ala Val
 260 265 270
 Ile Val Val Val Val Leu Ala Val Ile Ala Gly Ile Val Val Leu Val
 275 280 285
 Ile Ser Thr Arg Lys Arg Ser Ala Lys Tyr Glu Lys Ala Glu Ile Lys
 290 295 300
 Glu Met Gly Glu Ile His Arg Glu Leu Asn Ala
 305 310 315

<210> 5
 <211> 315
 <212> PRT
 <213> Rattus rattus

<400> 5

Met Ala Pro Pro Lys Ala Leu Ala Phe Gly Leu Leu Leu Ala Val Val
 1 5 10 15
 Thr Ala Thr Leu Ala Ala Ala Gln Lys Asp Cys Val Cys Asn Asn Tyr
 20 25 30
 Lys Leu Thr Ser Arg Cys Tyr Glu Asn Glu Asn Gly Glu Cys Gln Cys
 35 40 45
 Thr Ser Tyr Gly Thr Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ser
 50 55 60
 Lys Cys Leu Val Met Lys Ala Glu Met Thr His Ser Lys Ser Gly Arg
 65 70 75 80
 Arg Met Lys Pro Glu Gly Ala Ile Gln Asn Asn Asp Gly Leu Tyr Asp
 85 90 95
 Pro Glu Cys Asp Glu Gln Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
 100 105 110
 Thr Ala Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
 115 120 125
 Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
 130 135 140
 Ile Ile Glu Leu Lys His Lys Glu Arg Ala Gln Pro Tyr Asn Phe Glu
 145 150 155 160
 Ser Leu His Thr Ala Leu Gln Asp Thr Phe Ala Ser Arg Tyr Met Leu
 165 170 175
 Asn Pro Lys Phe Ile Lys Ser Ile Met Tyr Glu Asn Asn Val Ile Thr
 180 185 190
 Ile Asp Leu Met Gln Asn Ser Ser Gln Lys Thr Gln Asp Asp Val Asp
 195 200 205
 Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
 210 215 220
 Leu Phe His Ser Ser Lys Ser Met Asp Leu Arg Val Asn Gly Glu Leu
 225 230 235 240
 Leu Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys
 245 250 255
 Ala Pro Glu Phe Ser Met Gln Gly Leu Thr Ala Gly Ile Ile Ala Val
 260 265 270
 Ile Val Val Val Val Leu Ala Val Ile Ala Gly Ile Val Val Leu Val
 275 280 285
 Ile Ser Thr Arg Lys Arg Ser Ala Lys Tyr Glu Lys Ala Glu Ile Lys
 290 295 300

Glu Met Gly Glu Ile His Arg Glu Leu Asn Ala
 305 310 315

<210> 6
 <211> 314
 <212> PRT
 <213> Mus musculus

<400> 6
 Met Ala Gly Pro Gln Ala Leu Ala Phe Gly Leu Leu Leu Ala Val Val
 1 5 10 15
 Thr Ala Thr Leu Ala Ala Ala Gln Arg Asp Cys Val Cys Asp Asn Tyr
 20 25 30
 Lys Leu Ala Thr Ser Cys Ser Leu Asn Glu Tyr Gly Glu Cys Gln Cys
 35 40 45
 Thr Ser Tyr Gly Thr Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ser
 50 55 60
 Lys Cys Leu Ala Met Lys Ala Glu Met Thr His Ser Lys Ser Gly Arg
 65 70 75 80
 Arg Ile Lys Pro Glu Gly Ile Gln Asn Asn Asp Gly Leu Tyr Asp Pro
 85 90 95
 Asp Cys Asp Glu Gln Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly Thr
 100 105 110
 Ala Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp Lys
 115 120 125
 Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile Ile
 130 135 140
 Ile Glu Leu Lys His Lys Glu Arg Glu Ser Pro Tyr Asp His Gln Ser
 145 150 155 160
 Leu Gln Thr Ala Leu Gln Glu Ala Phe Thr Ser Arg Tyr Lys Leu Asn
 165 170 175
 Gln Lys Phe Ile Lys Asn Ile Met Tyr Glu Asn Asn Val Ile Thr Ile
 180 185 190
 Asp Leu Met Gln Asn Ser Ser Gln Lys Thr Gln Asp Asp Val Asp Ile
 195 200 205
 Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser Leu
 210 215 220
 Phe His Ser Ser Lys Ser Met Asp Leu Arg Val Asn Gly Glu Pro Leu
 225 230 235 240
 Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
 245 250 255
 Pro Glu Phe Ser Met Gln Gly Leu Thr Ala Gly Ile Ile Ala Val Ile
 260 265 270
 Val Val Val Ser Leu Ala Val Ile Ala Gly Ile Val Val Leu Val Ile
 275 280 285
 Ser Thr Arg Lys Lys Ser Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
 290 295 300
 Met Gly Glu Ile His Arg Glu Leu Asn Ala
 305 310

<210> 7
 <211> 314
 <212> PRT
 <213> Homo sapien

<400> 7
 Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala

1 5 10 15
 Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
 20 25 30
 Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
 35 40 45
 Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
 50 55 60
 Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
 65 70 75 80
 Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
 85 90 95
 Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
 100 105 110
 Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
 115 120 125
 Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
 130 135 140
 Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
 145 150 155 160
 Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
 165 170 175
 Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
 180 185 190
 Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
 195 200 205
 Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
 210 215 220
 Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
 225 230 235 240
 Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
 245 250 255
 Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
 260 265 270
 Val Val Val Val Met Ala Val Val Ala Gly Ile Val Val Leu Val Ile
 275 280 285
 Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
 290 295 300
 Met Gly Glu Met His Arg Glu Leu Asn Ala
 305 310

<210> 8
 <211> 323
 <212> PRT
 <213> Homo sapien

<400> 8
 Met Ala Arg Gly Pro Gly Leu Ala Pro Pro Pro Leu Arg Leu Pro Leu
 1 5 10 15
 Leu Leu Leu Val Leu Ala Ala Val Thr Gly His Thr Ala Ala Gln Asp
 20 25 30
 Asn Cys Thr Cys Pro Thr Asn Lys Met Thr Val Cys Ser Pro Asp Gly
 35 40 45
 Pro Gly Gly Arg Cys Gln Cys Arg Ala Leu Gly Ser Gly Met Ala Val
 50 55 60
 Asp Cys Ser Thr Leu Thr Ser Lys Cys Leu Leu Leu Lys Ala Arg Met
 65 70 75 80
 Ser Ala Pro Lys Asn Ala Arg Thr Leu Val Arg Pro Ser Glu His Ala

85										90										95										
Leu	Val	Asp	Asn	Asp	Gly	Leu	Tyr	Asp	Pro	Asp	Cys	Asp	Pro	Glu	Gly															
			100					105					110																	
Arg	Phe	Lys	Ala	Arg	Gln	Cys	Asn	Gln	Thr	Ser	Val	Cys	Trp	Cys	Val															
		115					120					125																		
Asn	Ser	Val	Gly	Val	Arg	Arg	Thr	Asp	Lys	Gly	Asp	Leu	Ser	Leu	Arg															
	130					135					140																			
Cys	Asp	Asp	Leu	Val	Arg	Thr	His	His	Ile	Leu	Ile	Asp	Leu	Arg	His															
145					150					155				160																
Arg	Pro	Thr	Ala	Gly	Ala	Phe	Asn	His	Ser	Asp	Leu	Asp	Ala	Glu	Leu															
			165					170						175																
Arg	Arg	Leu	Phe	Arg	Glu	Arg	Tyr	Arg	Leu	His	Pro	Lys	Phe	Val	Ala															
		180					185						190																	
Ala	Val	His	Tyr	Glu	Gln	Pro	Thr	Ile	Gln	Ile	Glu	Leu	Arg	Gln	Asn															
	195					200					205																			
Thr	Ser	Gln	Lys	Ala	Ala	Gly	Glu	Val	Asp	Ile	Gly	Asp	Ala	Ala	Tyr															
	210					215					220																			
Tyr	Phe	Glu	Arg	Asp	Ile	Lys	Gly	Glu	Ser	Leu	Phe	Gln	Gly	Arg	Gly															
225					230					235				240																
Gly	Leu	Asp	Leu	Arg	Val	Arg	Gly	Glu	Pro	Leu	Gln	Val	Glu	Arg	Thr															
			245					250					255																	
Leu	Ile	Tyr	Tyr	Leu	Asp	Glu	Ile	Pro	Pro	Lys	Phe	Ser	Met	Lys	Arg															
		260					265						270																	
Leu	Thr	Ala	Gly	Leu	Ile	Ala	Val	Ile	Val	Val	Val	Val	Val	Ala	Leu															
	275					280							285																	
Val	Ala	Gly	Met	Ala	Val	Leu	Val	Ile	Thr	Asn	Arg	Arg	Lys	Ser	Gly															
	290					295					300																			
Lys	Tyr	Lys	Lys	Val	Glu	Ile	Lys	Glu	Leu	Gly	Glu	Leu	Arg	Lys	Glu															
305					310					315				320																
Pro	Ser	Leu																												